

[illegible]

(2) INFORMATION FOR SEQ ID NO:1:

- CTATCCTTTT GTTTTCCATC CTG

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCCCTGCCTT TTCCAGCAAC GGT

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCTCCAGGAT AAAAGGCCAC GGT

23

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TACATTGGAA AATTTTATTA CAC

23

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGAAAAACAA

10

(2) INFORMATION FOR SEQ ID NO:6:

0905147-041698

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGGAAAAGGC

10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGGATAAAAG

10

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 902 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Ala Ala Ser Cys Glu Asp Glu Glu Leu Glu Phe Leu Leu Val  
 1 5 10 15

Phe Gly Glu Glu Leu Glu Ala Pro Pro Leu Gly Ala Gly Gly Leu Gly  
 20 25 30

Glu Glu Leu Asp Ser Glu Asp Ala Pro Pro Cys Cys Arg Leu Ala Leu  
 35 40 45

Gly Glu Pro Pro Pro Tyr Gly Ala Ala Pro Ile Gly Ile Pro Arg Pro  
 50 55 60

Pro Pro Pro Arg Pro Gly Met His Ser Pro Pro Pro Arg Pro Ala Pro  
 65 70 75 80

Ser Pro Gly Thr Trp Glu Ser Gln Pro Ala Arg Ser Val Arg Leu Gly  
 85 90 95

Gly Pro Gly Gly Gly Ala Gly Gly Ala Gly Gly Gly Arg Val Leu Glu

09061417-041698

09061417 04169B

100	105	110
Cys Pro Ser Ile Arg Ile Thr Ser Ile Ser Pro Thr Pro Glu Pro Pro 115 120 125		
Ala Ala Leu Glu Asp Asn Pro Asp Ala Trp Gly Asp Gly Ser Pro Arg 130 135 140		
Asp Tyr Pro Pro Pro Glu Gly Phe Gly Gly Tyr Arg Glu Ala Gly Ala 145 150 155 160		
Gln Gly Gly Gly Ala Phe Phe Ser Pro Ser Pro Gly Ser Ser Ser Leu 165 170 175		
Ser Ser Trp Ser Phe Phe Ser Asp Ala Ser Asp Glu Ala Ala Leu Tyr 180 185 190		
Ala Ala Cys Asp Glu Val Glu Ser Glu Leu Asn Glu Ala Ala Ser Arg 195 200 205		
Phe Gly Leu Gly Ser Pro Leu Pro Ser Pro Arg Ala Ser Pro Arg Pro 210 215 220		
Trp Thr Pro Glu Asp Pro Trp Ser Leu Tyr Gly Pro Ser Pro Gly Gly 225 230 235 240		
Arg Gly Pro Glu Asp Ser Trp Leu Leu Leu Ser Ala Pro Gly Pro Thr 245 250 255		
Pro Ala Ser Pro Arg Pro Ala Ser Pro Cys Gly Leu Arg Arg Tyr Ser 260 265 270		
Ser Ser Gly Thr Pro Ser Ser Ala Ser Pro Ala Leu Ser Arg Arg Gly 275 280 285		
Ser Leu Gly Glu Glu Gly Ser Glu Pro Pro Pro Pro Pro Pro Leu Pro 290 295 300		
Leu Ala Arg Asp Pro Gly Ser Pro Gly Pro Phe Asp Tyr Val Gly Ala 305 310 315 320		
Pro Pro Ala Glu Ser Ile Pro Gln Leu Thr Arg Arg Thr Ser Ser Glu 325 330 335		
Gln Ala Val Ala Leu Pro Arg Ser Glu Glu Pro Ala Ser Cys Asn Gly 340 345 350		
Leu Leu Pro Leu Gly Ala Glu Glu Ser Val Ala Pro Pro Gly Gly Ser 355 360 365		
Arg Lys Glu Val Ala Gly Met Asp Tyr Leu Ala Val Pro Ser Pro Leu 370 375 380		
Ala Trp Ser Leu Ala Arg Ile Gly Gly His Ser Pro Ile Phe Arg Thr		

09061417-041698

385		390		395		400
Ser Ala Leu Pro	Pro Leu Asp Trp Pro	Leu Pro Ser Gln Tyr Glu Gln				
	405	410				415
Leu Glu Leu Arg	Ile Glu Val Gln Pro Arg Ala His His Arg Ala His					
	420	425				430
Tyr Glu Thr Glu Gly Ser Arg Gly Ala Val Leu Ala Ala Pro Gly Gly						
	435	440				445
His Pro Val Val Leu Leu Leu Gly Tyr Ser Glu Leu Pro Leu Thr Leu						
	450	455				460
Gln Met Phe Ile Gly Thr Ala Asp Glu Arg Asn Leu Arg Pro His Ala						
	465	470			475	480
Phe Tyr Gln Val His Arg Ile Thr Gly Leu Met Val Ala Thr Ala Ser						
	485	490				495
Tyr Glu Ala Val Val Ser Gly Thr Leu Val Leu Glu Met Thr Leu Leu						
	500	505				510
Pro Glu Asn Asn Met Ala Ala Asn Ile Asp Cys Ala Gly Ile Leu Leu						
	515	520				525
Leu Arg Asn Ser Asp Ile Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly						
	530	535				540
Arg Lys Asn Thr Arg Val Arg Leu Val Phe Arg Val His Val Pro Gln						
	545	550			555	560
Gly Gly Gly Leu Val Val Ser Val Gln Ala Ala Ser Val Pro Ile Glu						
	565	570				575
Cys Ser Gln Arg Ser Ala Gln Glu Leu Pro Gln Val Glu Ala Tyr Ser						
	580	585				590
Pro Ser Ala Cys Ser Val Arg Gly Gly Glu Glu Leu Val Leu Thr Gly						
	595	600				605
Ser Asn Phe Leu Pro Asp Ser Leu Val Val Phe Ile Glu Arg Gly Pro						
	610	615				620
Asp Gly Leu Leu Gln Trp Glu Glu Glu Ala Thr Val Asn Arg Leu Gln						
	625	630			635	640
Ser Asn Glu Val Thr Leu Thr Leu Thr Val Pro Glu Tyr Ser Asn Leu						
	645	650				655
Arg Val Ser Arg Pro Val Gln Val Tyr Phe Tyr Val Ser Asn Gly Arg						
	660	665				670
Arg Lys Arg Ser Pro Thr Gln Ser Phe Arg Phe Leu Pro Val Ile Cys						

675	680	685
Leu Glu Glu Pro Leu Pro Asp Ser Ser Leu Arg Gly Phe Pro Ser Ala 690 695 700		
Ser Ala Thr Pro Phe Gly Thr Asp Met Asp Phe Ser Pro Pro Arg Pro 705 710 715 720		
Pro Tyr Pro Ser Tyr Pro His Glu Asp Pro Ala Cys Glu Thr Pro Tyr 725 730 735		
Leu Ser Glu Gly Phe Gly Tyr Gly Met Pro Pro Leu Tyr Pro Gln Thr 740 745 750		
Gly Pro Pro Pro Ser Tyr Arg Pro Gly Leu Arg Met Phe Pro Glu Thr 755 760 765		
Arg Gly Thr Thr Gly Cys Ala Gln Pro Pro Ala Val Ser Phe Leu Pro 770 775 780		
Arg Pro Phe Pro Ser Asp Pro Tyr Gly Gly Arg Gly Ser Ser Phe Pro 785 790 795 800		
Leu Gly Leu Pro Phe Ser Pro Pro Ala Pro Phe Arg Pro Pro Pro Leu 805 810 815		
Pro Ala Ser Pro Pro Leu Glu Gly Pro Phe Pro Ser Gln Ser Asp Val 820 825 830		
His Pro Leu Pro Ala Glu Gly Tyr Asn Leu Val Gly Pro Gly Tyr Gly 835 840 845		
Pro Gly Glu Gly Ala Pro Glu Gln Glu Leu Ser Arg Gly Gly Tyr Ser 850 855 860		
Ser Gly Phe Arg Asp Ser Val Pro Ile Gln Gly Ile Thr Leu Glu Glu 865 870 875 880		
Val Ser Glu Ile Ile Gly Arg Asp Leu Ser Gly Phe Pro Ala Pro Pro 885 890 895		
Gly Glu Glu Pro Pro Ala 900		

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTTCTGGAG	GGAGGCGGCA	GCGACGGAGG	AGGGGGCTTC	TCAGAGAAAG	GGAGGGAGGG	60
AGCCACCCGG	GTGAAGATAC	AGCAGCCTCC	TGAACTCCCC	CCTCCCACCC	AGGCCGGGAC	120
CTGGGGGCTC	CTGCCGGATC	CATGGGGGCG	GCCAGCTGCG	AGGATGAGGA	GCTGGAATTT	180
AAGCTGGTGT	TCGGGGAGGA	AAAGGAGGCC	CCCCCGCTGG	GCGCGGGGGG	ATTGGGGGAA	240
GAAGTGGACT	CAGAGGATGC	CCCGCCATGC	TGCCGTCTGG	CCTTGGGAGA	GCCCCCTCCC	300
TATGGCGCTG	CACCTATCGG	TATTCCCCGA	CCTCCACCCC	CTCGGCCTGG	CATGCATTCTG	360
CCACCGCCGC	GACCAGCCCC	CTCACCTGGC	ACCTGGGAGA	GCCAGCCCGC	CAGGTCGGTG	420
AGGCTGGGAG	GACCAGGAGG	GGGTGCTGGG	GGTGCTGGGG	GTGGCCGTGT	TCTCGAGTGT	480
CCCAGCATCC	GCATCACCTC	CATCTCTCCC	ACGCCGGAGC	CGCCAGCAGC	GCTGGAGGAC	540
AACCCTGATG	CCTGGGGGGA	CGGCTCTCCT	AGAGATTACC	CCCCACCAGA	AGGCTTTGGG	600
GGCTACAGAG	AAGCAGGGGC	CCAGGGTGGG	GGGGCCTTCT	TCAGCCCAAG	CCCTGGCAGC	660
AGCAGCCTGT	CCTCGTGGAG	CTTCTTCTCC	GATGCCTCTG	ACGAGGCAGC	CCTGTATGCA	720
GCCTGCGACG	AGGTGGAGTC	TGAGCTAAAT	GAGGCGGCCT	CCCGCTTTGG	CCTGGGCTCC	780
CCGCTGCCCT	CGCCCCGGGC	CTCCCCCTCG	CCATGGACCC	CCGAAGATCC	CTGGAGCCTG	840
TATGGTCCAA	GCCCCGGAGG	CCGAGGGCCA	GAGGATAGCT	GGCTACTCCT	CAGTGCTCCT	900
GGGCCCACCC	CAGCCTCCCC	GCGGCCTGCC	TCTCCATGTG	GCAAGCGGCG	CTATTCCAGC	960
TCGGGAACCC	CATCTTCAGC	CTCCCCAGCT	CTGTCCCGCC	GTGGCAGCCT	GGGGGAAGAG	1020
GGGTCTGAGC	CACCTCCACC	ACCCCCATTG	CCTCTGGCCC	GGGACCCGGG	CTCCCCCTGGT	1080
CCCTTTGACT	ATGTGGGGGC	CCCACCAGCT	GAGAGCATCC	CTCAGAAGAC	ACGGCGGACT	1140
TCCAGCGAGC	AGGCAGTGGC	TCTGCCTCGG	TCTGAGGAGC	CTGCCTCATG	CAATGGGAAG	1200
CTGCCCTTGG	GAGCAGAGGA	GTCTGTGGCT	CCTCCAGGAG	GTTCCCGGAA	GGAGGTGGCT	1260
GGCATGGACT	ACCTGGCAGT	GCCCTCCCCA	CTCGCTTGGT	CCAAGGCCCG	GATTGGGGGA	1320
CACAGCCCTA	TCTTCAGGAC	CTCTGCCCTA	CCCCCACTGG	ACTGGCCTCT	GCCCAGCCAA	1380
TATGAGCAGC	TGGAGCTGAG	GATCGAGGTA	CAGCCTAGAG	CCCACCACCG	GGCCCACTAT	1440
GAGACAGAAG	GCAGCCGTGG	AGCTGTCAAA	GCTGCCCTTG	GCGGTCACCC	CGTAGTCAAG	1500
CTCCTAGGCT	ACAGTGAGAA	GCCACTGACC	CTACAGATGT	TCATCGGCAC	TGCAGATGAA	1560
AGGAACCTGC	GGCCTCATGC	CTTCTATCAG	GTGCACCGTA	TCACAGGCAA	GATGGTGGCC	1620

